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Figure 4. The *CaESS1* gene of *Candida albicans*.

1 GATCAACCAATAGATGTTGTTGCTAACCAAGTCAAAGACGCGTTGAAGACAGAGGTATTACACACACAAGCATTATGTCAGTTGAAT RR
 189 AGATATACAGCTTGAGATTCCCTCTCCCAATACATATTACCTACTGTACATTTACCAAAACTCTCTCTTTTCTATATTTCTTCATCAACACAGATTTTC 180
 189 GTTGTGCTCCCTTTTGTGTATATTTGTCTACATTTAGCTTGAATCTTTTTCAGTATATATATCATC ATG GCA TCG ACA TCA ACA GGC TTA 279
 1 H A S T S T G L B
 280 GCA CTT AAT TGG AGI ATT AGA GTA TCC AGA TCC CAT AAC AAA GAG TAT TTC TTA AAC CAA TCT ACC AAT GAG TCG 354
 9 P P N W T I R V S R S H N K E Y F L N Q S T N R H 33
 355 TCT TGG GAC CCA CTT TAT GGC ACT GAC AAA GAA GTA TTG AAT GCA TAC ATT GCG AAG TTT AAA AAC AAT GGT TAC 429
 34 S W D P P Y G T D K E V L N A Y I A K E K N N G Y 58
 430 AAG CCA CTT GTC AAT GAG CAT GGC CAG GTT ACA GTT TCT CAT TTG TTG ATC AAG AAC AAT CAA TCA AGA AAA CCC 504
 59 K P L V N E D G Q V R V S H L I I K N N Q S R K D 83
 505 AAG TCT TGG AAG TCC CCA GAT GGT ATA AGT AGA ACT AGA GAC GAA TCT ATA CAG ATA TTG AAG AAA CAT TTG GAA 579
 84 K S W K S P D G I S R T R D E S I Q I L K K H L R 108
 580 AGA ATA TTG AGT GGT GAG GPT AAA CTA AGT GAA TTG GCA AAT ACC GAA AGT GAT TOC ACC TCA CAT GAC AGA GGT 654
 109 K I L G G E V K L S E L A N T R S D C S S H D R G 133
 655 GGT GAT TTA GGG TTT TTT AGC AAA GGA CAA ATG CAA CCA CCA TTC GAA GAA GCU GCA TTC AAT TTG CAT CTT GGA 729
 134 C D L G F F S K C Q M Q P F F E E A A F N L H V O 150
 730 GAA GTC AGT AAC ATA ATT GAA ACC AAT AGT GGT GTC CAT ATC CTC CAA AGA ACA GGA TAA ATCAAGATATTGGACTTTGA 809
 159 K V S N I I K T N S G V H I L Q R T O 178
 810 TGAATAATGAATAAATAGACAGCAACTCTATAGATTTCCTAACCAAAAAGCGATGGCTCACAAAAGTCGAAAATCTGAGAGCAACATCTTACCAG 908
 910 TACACGGCGATTAAGACTCTAATTCGATATTTATATAATGGGAACGTTCCCGTCATTGGTTTGTATATTGGATCC 989

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Figure 4. Complete nucleotide sequence of the *CaESS1* gene from *Candida albicans* and its predicted translation product. The *CaESS1*-encoded protein is 177 amino acids long and has a predicted MW of 19.8 Kd. It is 42% identical to the *ESS1* protein of *Saccharomyces cerevisiae*.

Figure 1B. Gene Knockout of *CaESS1* in *Candida albicans*.

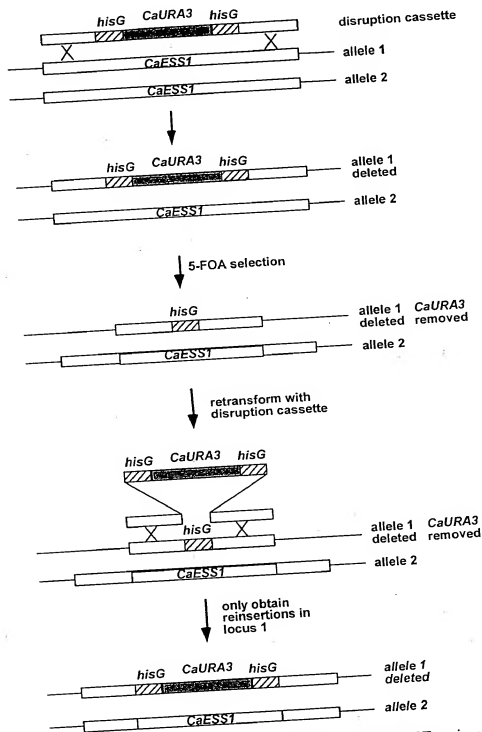
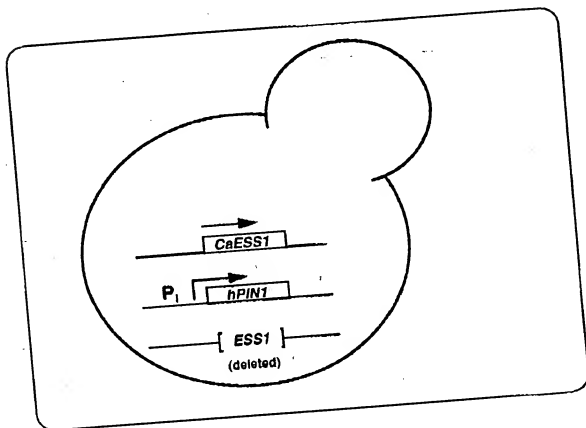


Figure 1B. *CaEss1* was deleted in strain CA14 by the method of Fonzi and Irwin (1993). *Ura*⁺ transformants were selected, genomic DNA was prepared and analyzed by Southern hybridization and by PCR. Results confirmed homologous recombination and gene deletion of the first allele as outlined in the figure. The *CaURA3* gene was then removed by selection with 5-FOA, and diploid disruption strains (*caess1/CaESS1*) were used for retransformation with the *hisG*-*CaURA3*-*hisG*/*CaESS1* disruption cassette as before. No homozygous deletion strains (*caess1/caess1*) were obtained (see Table 1). Instead the *hisG*-*CaURA3*-*hisG*/*CaESS1* cassette reinserted into the already disrupted allele in all *Ura*⁺ transformants analyzed.

Figure 2. Yeast Strain to Identify Inhibitors
Specific for *Candida albicans* CaESS1



00507242-021600

Figure 3. Screen for *CaESS1* Inhibitors

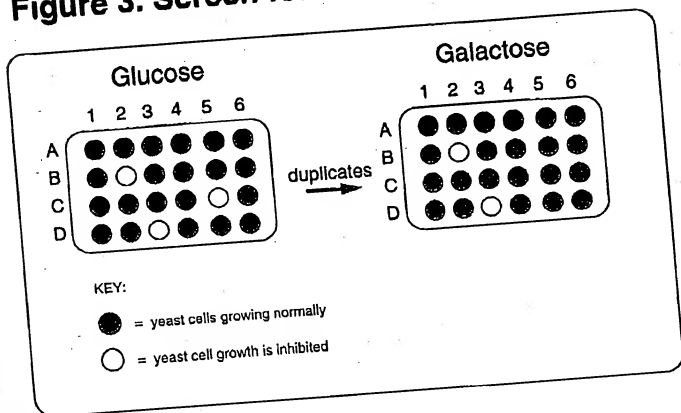
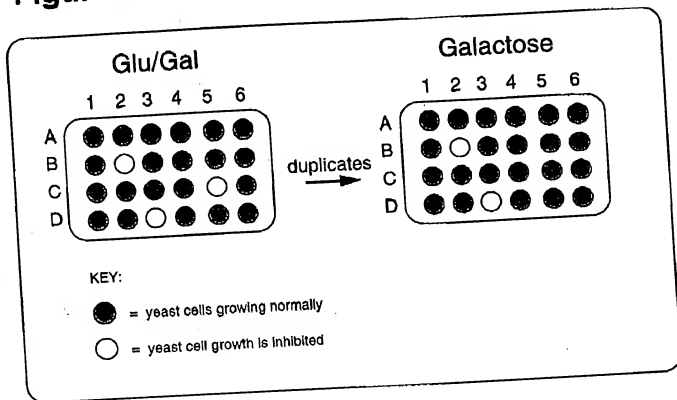


Figure 4. Screen for *hPIN1* Inhibitors

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